

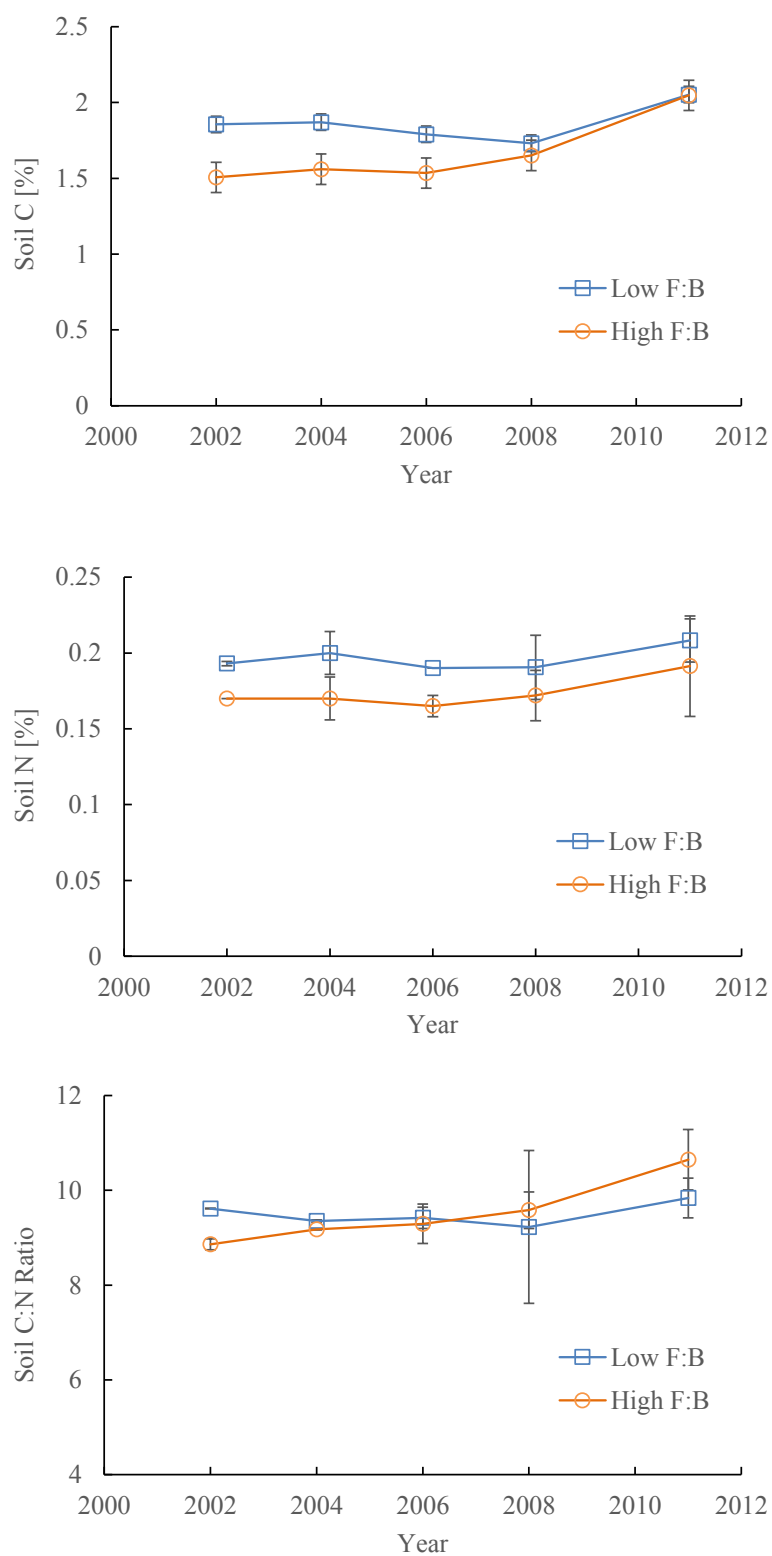
## *Supplementary Material*

### **Soil fungal:bacterial ratios are linked to altered carbon cycling**

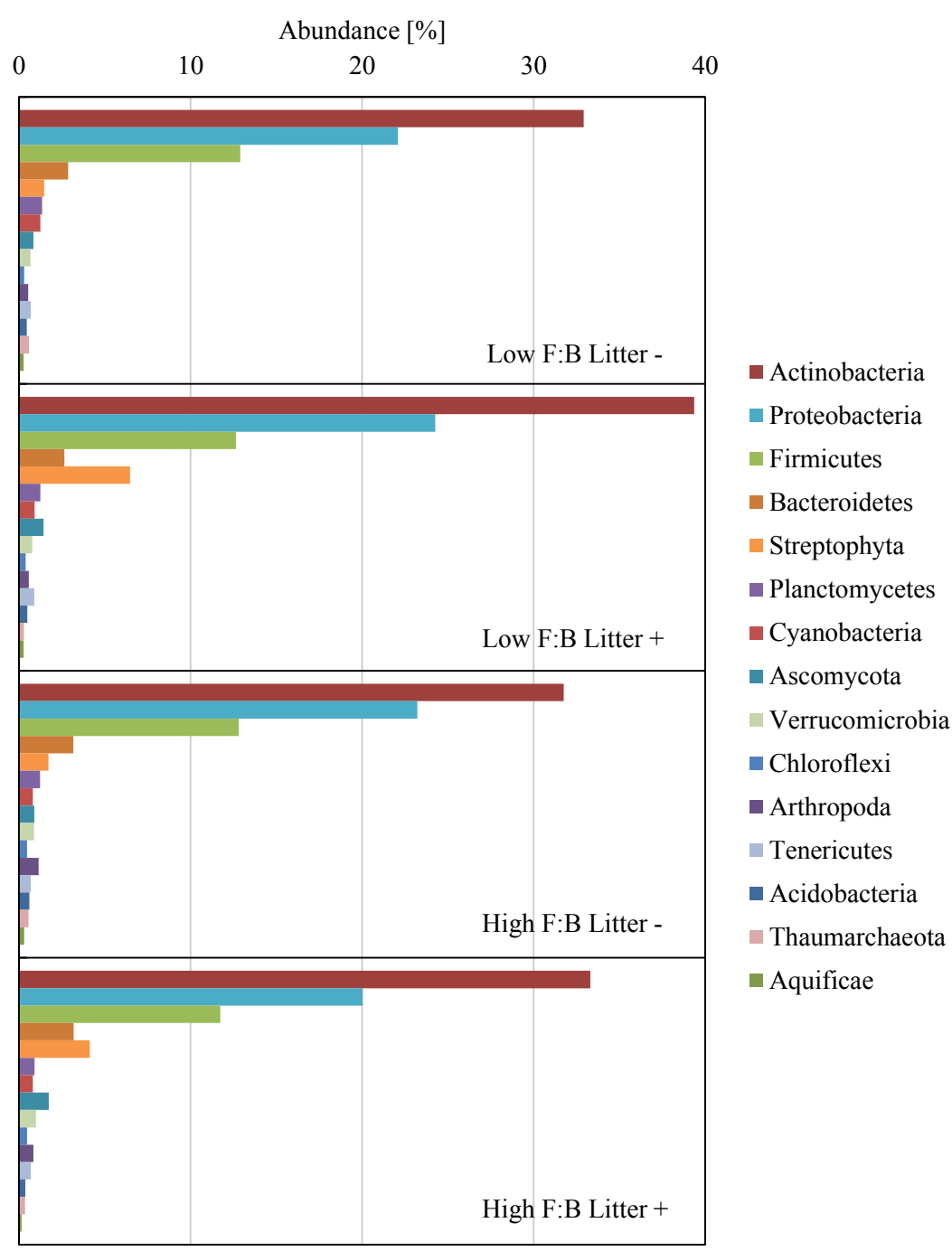
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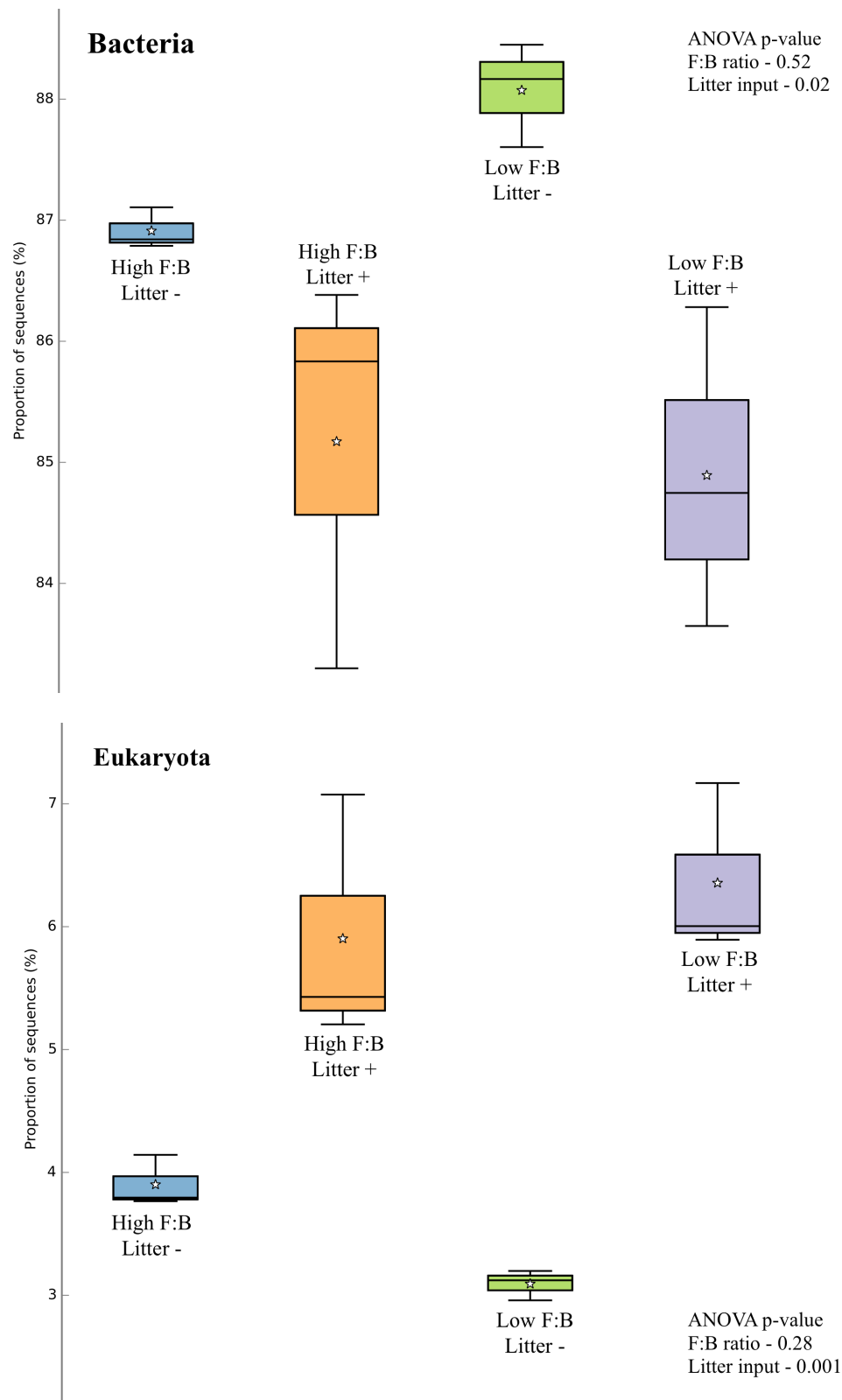
## Supplementary Figures

**Figure S-1:** Organic C, N and C:N ratio of the soils (0-10 cm depth) used in the experiment.

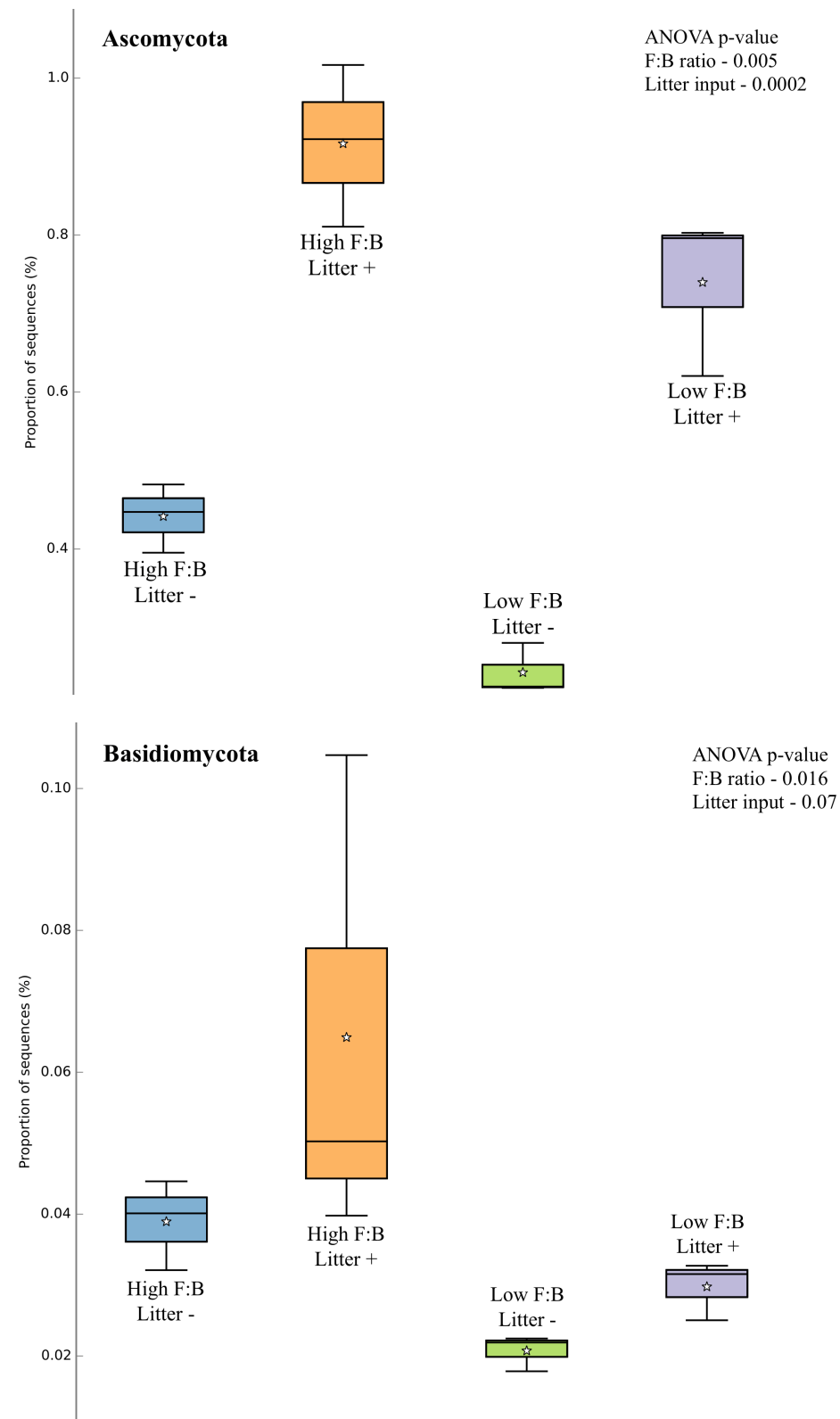
**Figure S-2:** Relative abundance of the major phyla in the two soils and the shifts on litter addition obtained using RNA-Seq based taxonomic classification



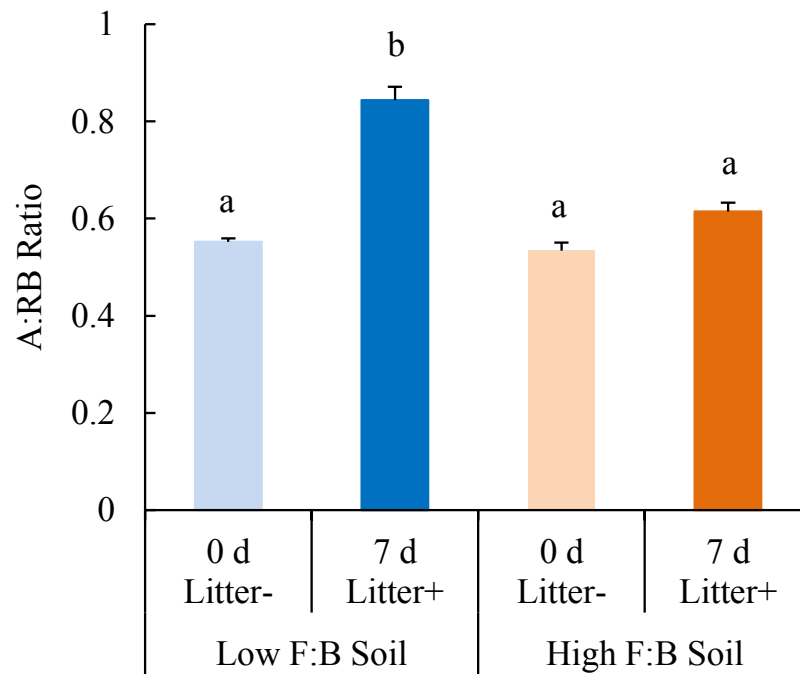
**Figure S-3:** RNA-Seq derived relative abundance of bacterial and eukaryotic domains in the two soils and their shift on litter addition. Global effect of F:B ratio and litter addition was assessed by repeated measures ANOVA.



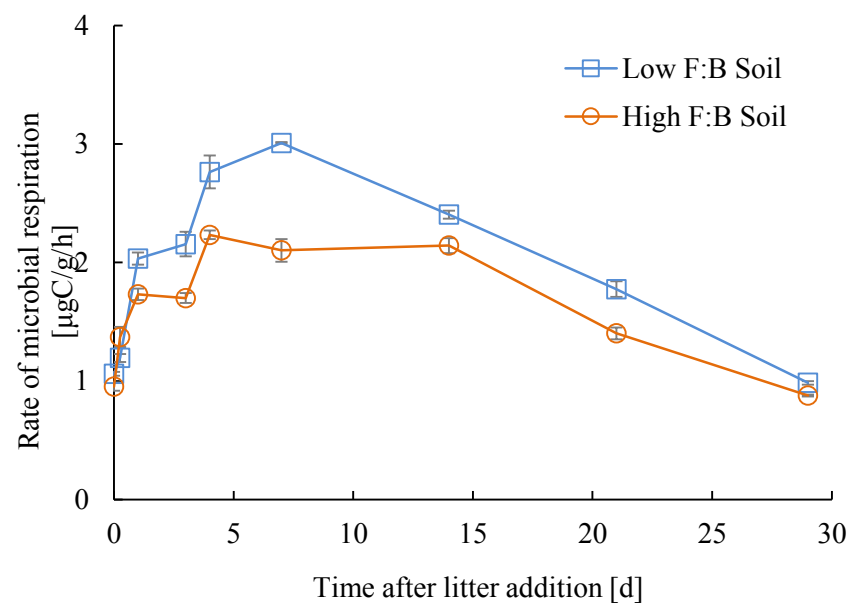
**Figure S-4:** RNA-Seq derived relative abundance of major fungal phyla in the two soils and their shift on litter addition. Global effect of F:B ratio and litter addition was assessed by repeated measures ANOVA.



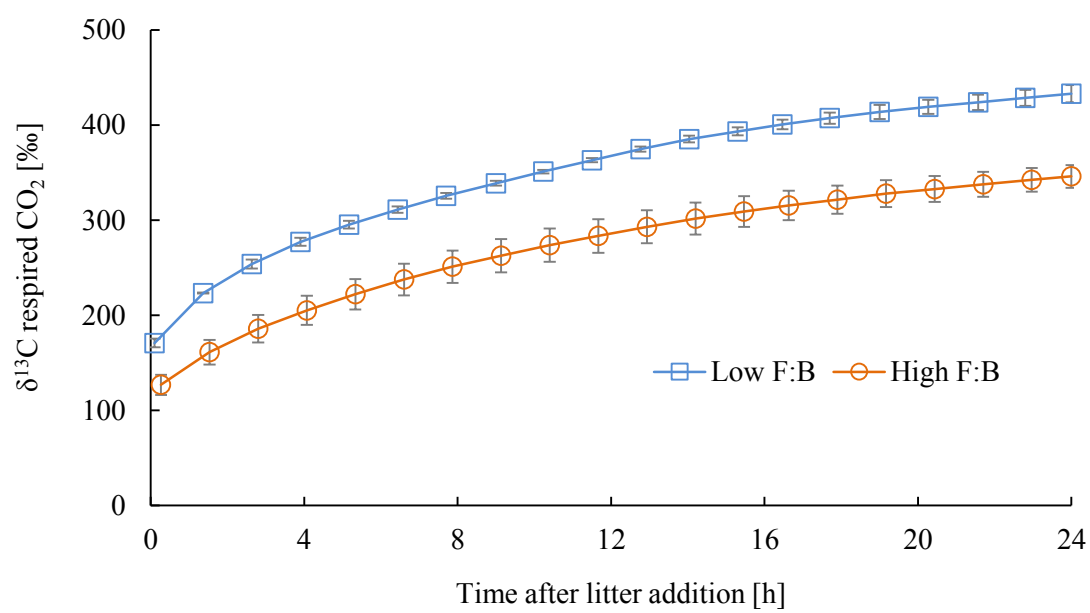
**Figure S-5:** Actinobacteria: rest of bacteria (A:RB) ratio estimated using RNA-Seq. Error bars represent standard error (n=3), lowercase letters from Fischer LSD test; treatments sharing a letter are not significant.



**Figure S-6:** Temporal trend in the rate microbial respiration. Note: error bars represent standard error; n=3.



**Figure S-7:**  $\delta^{13}\text{C}$  excess in microbial respired  $\text{CO}_2$  and its temporal trend over the first 24h after litter addition. Note: error bars represent standard error; n=3.



**Figure S-8:** Shifts in abundance of different COG/KOG functional groups after litter addition at different time points obtained using: (A) RNA-Seq: error bars represent standard error (n=3), and (B) Proteomics, values were derived from composite samples of replicates at each time point.

